

OIKE

## RAW SEQUENCE LISTING

DATE: 07/07/2001

PATENT APPLICATION: US/09/758,269

TIME: 13:01:18

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Output Set: N:\CRF3\07062001\I758269.raw

3 <110> APPLICANT: IUCHI, SATOSHI  
 4 KOBAYASHI, MASATOMO  
 5 SHINOZAKI, KAZUO  
 7 <120> TITLE OF INVENTION: TRANSGENIC PLANTS CARRYING NEOXANTHIN  
 8 CLEAVAGE ENZYME GENE  
 10 <130> FILE REFERENCE: 3914-3  
 12 <140> CURRENT APPLICATION NUMBER: 09/758,269  
 13 <141> CURRENT FILING DATE: 2001-01-12  
 15 <150> PRIOR APPLICATION NUMBER: JP 2001-003476  
 16 <151> PRIOR FILING DATE: 2001-01-11  
 18 <150> PRIOR APPLICATION NUMBER: JP 2000-010056  
 19 <151> PRIOR FILING DATE: 2000-01-13  
 21 <160> NUMBER OF SEQ ID NOS: 33  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1752  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Arabidopsis thaliana  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (1)..(1749)  
 34 <400> SEQUENCE: 1

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37	1 5 10 15	
39	cct caa gcc caa att gat ttg ggt ttt agg ccc att aaa aga caa ccg	96
40	Pro Gln Ala Gln Ile Asp Leu Gly Phe Arg Pro Ile Lys Arg Gln Pro	
41	20 25 30	
43	aag gtt att aaa tgc acg gtg cag atc gac gta acg gaa tta acc aaa	144
44	Lys Val Ile Lys Cys Thr Val Gln Ile Asp Val Thr Glu Leu Thr Lys	
45	35 40 45	
47	aaa cgc caa tta ttt aca ccc aga acc acc gct act ccg ccg cag cat	192
48	Lys Arg Gln Leu Phe Thr Pro Arg Thr Thr Ala Thr Pro Pro Gln His	
49	50 55 60	
51	aat cct ctc cgg cta aac atc ttc cag aaa gcg gcg gcg att gcg atc	240
52	Asn Pro Leu Arg Leu Asn Ile Phe Gln Lys Ala Ala Ala Ile Ala Ile	
53	65 70 75 80	
55	gac gcg gct gag cgt gca tta atc tca cac gag caa gat tct cca ctt	288
56	Asp Ala Ala Glu Arg Ala Leu Ile Ser His Glu Gln Asp Ser Pro Leu	
57	85 90 95	
59	ccc aaa acc gct gat cca cgt gtt cag att gcc ggg aat tat tcc ccg	336
60	Pro Lys Thr Ala Asp Pro Arg Val Gln Ile Ala Gly Asn Tyr Ser Pro	
61	100 105 110	
63	gta ccg gaa tct tcc gtc cgg cga aac ctc acc gtc gaa gga aca atc	384
64	Val Pro Glu Ser Ser Val Arg Arg Asn Leu Thr Val Glu Gly Thr Ile	
65	115 120 125	
67	cct gac tgc att gac ggt gtt tat atc cgt aac ggc gcg aat ccg atg	432

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72 Phe Glu Pro Thr Ala Gly His His Leu Phe Asp Gly Asp Gly Met Val
73 145      150      155      160
75 cac gca gtt aaa ata acc aac ggt tca gct agc tac gca tgc cgg ttt      528
76 His Ala Val Lys Ile Thr Asn Gly Ser Ala Ser Tyr Ala Cys Arg Phe
77      165      170      175
79 aca aaa acc gag aga ttg gtt cag gaa aaa cga ttg ggt cga cca gtt      576
80 Thr Lys Thr Glu Arg Leu Val Gln Glu Lys Arg Leu Gly Arg Pro Val
81      180      185      190
83 ttc ccg aaa gca atc ggc gag ctt cac ggt cac tcg gga atc gca cgt      624
84 Phe Pro Lys Ala Ile Gly Glu Leu His Gly His Ser Gly Ile Ala Arg
85      195      200      205
87 ttg atg ctg ttt tac gca cgt ggg ctt tgt ggt ctg atc aac aac caa      672
88 Leu Met Leu Phe Tyr Ala Arg Gly Leu Cys Gly Leu Ile Asn Asn Gln
89      210      215      220
91 aac ggc gtc gga gta gca aac gcc ggt ttg gtt tac ttt aat aac cgg      720
92 Asn Gly Val Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn Asn Arg
93 225      230      235      240
95 ctt tta gct atg tca gaa gac gat tta ccg tac caa tta aaa att act      768
96 Leu Leu Ala Met Ser Glu Asp Asp Leu Pro Tyr Gln Leu Lys Ile Thr
97      245      250      255
99 caa acc ggc gat ctc caa acc gtt gga cgt tac gat ttc gac ggt cag      816
100 Gln Thr Gly Asp Leu Gln Thr Val Gly Arg Tyr Asp Phe Asp Gly Gln
101      260      265      270
103 tta aaa tcc gca atg ata gct cac ccg aaa ctg gac ccg gtt acg aag      864
104 Leu Lys Ser Ala Met Ile Ala His Pro Lys Leu Asp Pro Val Thr Lys
105      275      280      285
107 gag ctt cac gcg tta agc tac gac gtc gtt aag aaa cct tac ctg aaa      912
108 Glu Leu His Ala Leu Ser Tyr Asp Val Val Lys Lys Pro Tyr Leu Lys
109      290      295      300
111 tac ttc aga ttc tcg cca gac ggc gtt aaa tcg ccg gaa ttg gag atc      960
112 Tyr Phe Arg Phe Ser Pro Asp Gly Val Lys Ser Pro Glu Leu Glu Ile
113 305      310      315      320
115 ccg ctc gaa act ccg acg atg att cac gat ttc gct ata acg gag aat      1008
116 Pro Leu Glu Thr Pro Thr Met Ile His Asp Phe Ala Ile Thr Glu Asn
117      325      330      335
119 ttt gtg gtg att cct gat caa caa gtc gtg ttc aag ctc ggc gag atg      1056
120 Phe Val Val Ile Pro Asp Gln Gln Val Val Phe Lys Leu Gly Glu Met
121      340      345      350
123 att tcc ggt aaa tct ccg gtt gtt ttc gac gga gaa aag gtt tcc cga      1104
124 Ile Ser Gly Lys Ser Pro Val Val Phe Asp Gly Glu Lys Val Ser Arg
125      355      360      365
127 ttg ggg ata atg ccc aag gac gcg aca gaa gct tct cag ata atc tgg      1152
128 Leu Gly Ile Met Pro Lys Asp Ala Thr Glu Ala Ser Gln Ile Ile Trp
129      370      375      380
131 gtg aac tct ccg gag acg ttc tgt ttt cat ctc tgg aat gca tgg gaa      1200
132 Val Asn Ser Pro Glu Thr Phe Cys Phe His Leu Trp Asn Ala Trp Glu

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133 385          390          395          400
135 tcg ccg gag acg gag gag att gtg gtg atc gga tcg tgt atg tcg ccg 1248
136 Ser Pro Glu Thr Glu Glu Ile Val Val Ile Gly Ser Cys Met Ser Pro
137          405          410          415
139 gcg gat tca atc ttc aac gag aga gac gag agc ttg aga agc gtt ttg 1296
140 Ala Asp Ser Ile Phe Asn Glu Arg Asp Glu Ser Leu Arg Ser Val Leu
141          420          425          430
143 tcg gag atc agg ata aac ctc aga aca cgt aaa acc acg cgt cgt tcg 1344
144 Ser Glu Ile Arg Ile Asn Leu Arg Thr Arg Lys Thr Thr Arg Arg Ser
145          435          440          445
147 ttg ttg gtt aac gag gat gta aat tta gag att ggt atg gtt aac ccg 1392
148 Leu Leu Val Asn Glu Asp Val Asn Leu Glu Ile Gly Met Val Asn Arg
149          450          455          460
151 aac ccg tta gga aga aaa acc ccg ttc gcg ttt ttg gct att gct tat 1440
152 Asn Arg Leu Gly Arg Lys Thr Arg Phe Ala Phe Leu Ala Ile Ala Tyr
153 465          470          475          480
155 cct tgg cca aaa gtt tcc ggt ttc gct aag gtc gat ctt tgc acc ggt 1488
156 Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu Cys Thr Gly
157          485          490          495
159 gag atg aaa aaa tat att tac ggc ggt gag aaa tat ggc ggc gaa ccg 1536
160 Glu Met Lys Lys Tyr Ile Tyr Gly Gly Glu Lys Tyr Gly Gly Glu Pro
161          500          505          510
163 ttt ttc ttg ccc ggc aac tcc ggt aac ggc gaa gaa aat gaa gat gac 1584
164 Phe Phe Leu Pro Gly Asn Ser Gly Asn Gly Glu Glu Asn Glu Asp Asp
165          515          520          525
167 ggt tat ata ttt tgt cac gtt cat gac gaa gaa aca aag aca tca gag 1632
168 Gly Tyr Ile Phe Cys His Val His Asp Glu Glu Thr Lys Thr Ser Glu
169          530          535          540
171 ctt cag att att aac gct gtt aat tta aag ctt gaa gct acg att aaa 1680
172 Leu Gln Ile Ile Asn Ala Val Asn Leu Lys Leu Glu Ala Thr Ile Lys
173 545          550          555          560
175 cta ccg tct aga gta ccg tat ggg ttt cat ggc aca ttt gtg gat tcg 1728
176 Leu Pro Ser Arg Val Pro Tyr Gly Phe His Gly Thr Phe Val Asp Ser
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186 <212> TYPE: PRT
187 <213> ORGANISM: Arabidopsis thaliana
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193 Pro Gln Ala Gln Ile Asp Leu Gly Phe Arg Pro Ile Lys Arg Gln Pro
194 20 25 30
196 Lys Val Ile Lys Cys Thr Val Gln Ile Asp Val Thr Glu Leu Thr Lys
197 35 40 45
199 Lys Arg Gln Leu Phe Thr Pro Arg Thr Thr Ala Thr Pro Pro Gln His

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202 Asn Pro Leu Arg Leu Asn Ile Phe Gln Lys Ala Ala Ala Ile Ala Ile
203 65      70      75      80
205 Asp Ala Ala Glu Arg Ala Leu Ile Ser His Glu Gln Asp Ser Pro Leu
206      85      90      95
208 Pro Lys Thr Ala Asp Pro Arg Val Gln Ile Ala Gly Asn Tyr Ser Pro
209      100      105      110
211 Val Pro Glu Ser Ser Val Arg Arg Asn Leu Thr Val Glu Gly Thr Ile
212      115      120      125
214 Pro Asp Cys Ile Asp Gly Val Tyr Ile Arg Asn Gly Ala Asn Pro Met
215      130      135      140
217 Phe Glu Pro Thr Ala Gly His His Leu Phe Asp Gly Asp Gly Met Val
218 145      150      155      160
220 His Ala Val Lys Ile Thr Asn Gly Ser Ala Ser Tyr Ala Cys Arg Phe
221      165      170      175
223 Thr Lys Thr Glu Arg Leu Val Gln Glu Lys Arg Leu Gly Arg Pro Val
224      180      185      190
226 Phe Pro Lys Ala Ile Gly Glu Leu His Gly His Ser Gly Ile Ala Arg
227      195      200      205
229 Leu Met Leu Phe Tyr Ala Arg Gly Leu Cys Gly Leu Ile Asn Asn Gln
230      210      215      220
232 Asn Gly Val Gly Val Ala Asn Ala Gly Leu Val Tyr Phe Asn Asn Arg
233 225      230      235      240
235 Leu Leu Ala Met Ser Glu Asp Asp Leu Pro Tyr Gln Leu Lys Ile Thr
236      245      250      255
238 Gln Thr Gly Asp Leu Gln Thr Val Gly Arg Tyr Asp Phe Asp Gly Gln
239      260      265      270
241 Leu Lys Ser Ala Met Ile Ala His Pro Lys Leu Asp Pro Val Thr Lys
242      275      280      285
244 Glu Leu His Ala Leu Ser Tyr Asp Val Val Lys Lys Pro Tyr Leu Lys
245      290      295      300
247 Tyr Phe Arg Phe Ser Pro Asp Gly Val Lys Ser Pro Glu Leu Glu Ile
248 305      310      315      320
250 Pro Leu Glu Thr Pro Thr Met Ile His Asp Phe Ala Ile Thr Glu Asn
251      325      330      335
253 Phe Val Val Ile Pro Asp Gln Gln Val Val Phe Lys Leu Gly Glu Met
254      340      345      350
256 Ile Ser Gly Lys Ser Pro Val Val Phe Asp Gly Glu Lys Val Ser Arg
257      355      360      365
259 Leu Gly Ile Met Pro Lys Asp Ala Thr Glu Ala Ser Gln Ile Ile Trp
260      370      375      380
262 Val Asn Ser Pro Glu Thr Phe Cys Phe His Leu Trp Asn Ala Trp Glu
263 385      390      395      400
265 Ser Pro Glu Thr Glu Glu Ile Val Val Ile Gly Ser Cys Met Ser Pro
266      405      410      415
268 Ala Asp Ser Ile Phe Asn Glu Arg Asp Glu Ser Leu Arg Ser Val Leu
269      420      425      430
271 Ser Glu Ile Arg Ile Asn Leu Arg Thr Arg Lys Thr Thr Arg Arg Ser
272      435      440      445

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274 Leu Leu Val Asn Glu Asp Val Asn Leu Glu Ile Gly Met Val Asn Arg
275      450      455      460
277 Asn Arg Leu Gly Arg Lys Thr Arg Phe Ala Phe Leu Ala Ile Ala Tyr
278 465      470      475      480
280 Pro Trp Pro Lys Val Ser Gly Phe Ala Lys Val Asp Leu Cys Thr Gly
281      485      490      495
283 Glu Met Lys Lys Tyr Ile Tyr Gly Gly Glu Lys Tyr Gly Gly Glu Pro
284      500      505      510
286 Phe Phe Leu Pro Gly Asn Ser Gly Asn Gly Glu Glu Asn Glu Asp Asp
287      515      520      525
289 Gly Tyr Ile Phe Cys His Val His Asp Glu Glu Thr Lys Thr Ser Glu
290      530      535      540
292 Leu Gln Ile Ile Asn Ala Val Asn Leu Lys Leu Glu Ala Thr Ile Lys
293 545      550      555      560
295 Leu Pro Ser Arg Val Pro Tyr Gly Phe His Gly Thr Phe Val Asp Ser
296      565      570      575
298 Asn Glu Leu Val Asp Gln Leu
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303 <211> LENGTH: 1788
304 <212> TYPE: DNA
305 <213> ORGANISM: Arabidopsis thaliana
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308 <221> NAME/KEY: CDS
309 <222> LOCATION: (1)..(1785)
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316 cat cac tct ctt ctt cgc cgc cga tct tcc tct cct act ctc ctc cgt 96
317 His His Ser Leu Leu Arg Arg Arg Ser Ser Ser Pro Thr Leu Leu Arg
318      20      25      30
320 atc aac tcc gcc gtc gtc gaa gaa cgt tct cca atc aca aac cca agc 144
321 Ile Asn Ser Ala Val Val Glu Glu Arg Ser Pro Ile Thr Asn Pro Ser
322      35      40      45
324 gac aac aat gat cgt cgt aac aaa ccc aaa aca ctc cac aac cga acc 192
325 Asp Asn Asn Asp Arg Arg Asn Lys Pro Lys Thr Leu His Asn Arg Thr
326      50      55      60
328 aat cac acc tta gtc tca tca cca ccg aaa ctc cga cca gaa atg act 240
329 Asn His Thr Leu Val Ser Ser Pro Pro Lys Leu Arg Pro Glu Met Thr
330      65      70      75      80
332 ctc gca aca gct ctc ttc acc acc gtc gaa gat gta atc aac acg ttc 288
333 Leu Ala Thr Ala Leu Phe Thr Thr Val Glu Asp Val Ile Asn Thr Phe
334      85      90      95
336 atc gat cca cct tca cgt cct tcc gtt gat cca aaa cat gtc ctc tct 336
337 Ile Asp Pro Pro Ser Arg Pro Ser Val Asp Pro Lys His Val Leu Ser
338      100      105      110
340 gat aac ttc gct cct gtc ctc gac gag ctt cct cca aca gac tgt gaa 384
341 Asp Asn Phe Ala Pro Val Leu Asp Glu Leu Pro Pro Thr Asp Cys Glu

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VERIFICATION SUMMARY

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